

Figure 1a

Variable Heavy Chain DNA

3077_VH1B (SEQ ID NO: 1):

```

(1)  CAGGTGCAAT TGGTTCAGAG CGGCGCGGAA GTGAAAAAAC CGGGCGCGAG
(51) CGTGAAAGTG AGCTGCAAAG CCTCCGGATA TACCTTTACT TCTTATTCTA
(101) TTAATTGGGT CCGCCAAGCC CCTGGGCAGG GTCTCGAGTG GATGGGCTAT
(151) ATCGATCCGA ATCGTGGCAA TACGAATTAC GCGCAGAAGT TTCAGGGCCG
(201) GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT ATGGAAGTGA
(251) GCAGCCTGCG TAGCGAAGAT ACGGCCGTGT ATTATTGCGC GCGTGAGTAT
(301) ATTTATTTTA TTCATGGTAT GCTTGATTTT TGGGGCCAAG GCACCCTGGT
(351) GACGGTTAGC TCA

```

3079_VH3 (SEQ ID NO: 2):

```

(1)  CAGGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
(51) CCTGCGTCTG AGCTGCGCGG CCTCCGGATT TACCTTTTCT AATTATGGTA
(101) TGCATTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
(151) ATCCGTTCTG ATGGTAGCTG GACCTATTAT GCGGATAGCG TGAAAGGCCG
(201) TTTTACCAT TACAGTGATA ATTGCAAAAA CACCCTGTAT CTGCAAATGA
(251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTACGTTAT
(301) TGGTCTAAGT CTCATGCTTC TGTTACTGAT TATTGGGGCC AAGGCACCTT
(351) GGTGACGGTT AGCTCA

```

3080_VH3 (SEQ ID NO: 3):

```

(1)  CAGGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
(51) CCTGCGTCTG AGCTGCGCGG CCTCCGGATT TACCTTTTCT TCTTATGGTA
(101) TGCATTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
(151) ATCTATTCTG ATGGTAGCAA TACCTTTTAT GCGGATAGCG TGAAAGGCCG
(201) TTTTACCAT TACAGTGATA ATTGCAAAAA CACCCTGTAT CTGCAAATGA
(251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTAATATG
(301) TATCGTTGGC CTTTTCATTA TTTTTTTGAT TATTGGGGCC AAGGCACCTT
(351) GGTGACGGTT AGCTCA

```

3100_VH 3 (SEQ ID NO: 4):

```

(1)  CAGGTGCAAT TGGTGGAAAG CGGCGGCGGC CTGGTGCAAC CGGGCGGCAG
(51) CCTGCGTCTG AGCTGCGCGG CCTCCGGATT TACCTTTTCT TCTAATGGTA
(101) TGTCTTGGGT GCGCCAAGCC CCTGGGAAGG GTCTCGAGTG GGTGAGCAAT
(151) ATCTCTTATC TTTCTAGCTC TACCTATTAT GCGGATAGCG TGAAAGGCCG
(201) TTTTACCAT TACAGTGATA ATTGCAAAAA CACCCTGTAT CTGCAAATGA
(251) ACAGCCTGCG TGCGGAAGAT ACGGCCGTGT ATTATTGCGC GCGTTTTTAT
(301) GGTTATTTTA ATTATGCTGA TGTTTGGGGC CAAGGCACCC TGGTGACGGT
(351) TAGCTCA

```

3077_1_VH1B (SEQ ID NO: 31):

```

(1)  CAGGTGCAAT TAGTCCAAAG TGGTGCGGAA GTGAAAAAAC CGGGCGCGAG
(51) CGTGAAAGTG AGCTGCAAAG CCTCCGGATA TACCTTTACT TCTTATTCTA

```

(101) TTAATTGGGT CCGCCAAGCC CCTGGGCAGG GTCTCGAGTG GATGGGCTAT
(151) ATCGATCCGA ATCGTGGCAA TACGAATTAC GCGCAGAAGT TTCAGGGCCG
(201) GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT ATGGAACTGA
(251) GCAGCCTGCG TAGCGAAGAT ACGGCCGTGT ATTATTGCGC GCGTGAGTAT
(301) ATTTATTTTA TTCATGGTAT GCTTGATTTT TGGGGCCAAG GCACCCTGGT
(351) GACGGTTAGC TCA

Figure 1b**Variable Heavy Chain Peptide**(CDR Regions in **Bold**)**3077_VH1B** (SEQ ID NO: 5):

(1) QVQLVQSGAE VKKPGASVKV SCKAS**GYTFT** **SYSINWVRQA** PGQGLEWMGY
(51) **IDPNRGNTNY** **AQKFQGRVTM** TRDTSISTAY MELSSLRSED TAVYYCAREY
(101) **IYFIHGMLDF** WGQGTILVTVS S

3079_VH3 (SEQ ID NO: 6):

(1) QVQLVESGGG LVQPGGSLRL SCAAS**GFTFS** **NYGMHWVRQA** PGKGLEWVSN
(51) **IRSDGSWTYY** **ADSVKGRFTI** SRDNSKNTLY LQMNSLRAED TAVYYCARRY
(101) **WSKSHASVTD** YWGQGTILVTV SS

3080_VH3 (SEQ ID NO: 7):

(1) QVQLVESGGG LVQPGGSLRL SCAAS**GFTFS** **SYGMHWVRQA** PGKGLEWVSN
(51) **IYSDGSNTFY** **ADSVKGRFTI** SRDNSKNTLY LQMNSLRAED TAVYYCARNM
(101) **YRWPFIHYFFD** YWGQGTILVTV SS

3100_VH 3 (SEQ ID NO: 8):

(1) QVQLVESGGG LVQPGGSLRL SCAAS**GFTFS** **SNGMSWVRQA** PGKGLEWVSN
(51) **ISYLSSTYY** **ADSVKGRFTI** SRDNSKNTLY LQMNSLRAED TAVYYCARFY
(101) **GYFNYADVWG** QGTILVTVSS

Figure 2a**Variable Light Chain DNA****3077_Vk kappa 2 (SEQ ID NO: 9):**

```
(1)  GATATCGTGA TGACCCAGAG CCCACTGAGC CTGCCAGTGA CTCCGGGCGA
(51) GCCTGCGAGC ATTAGCTGCA GAAGCAGCCA AAGCCTGCTT TTTATTGATG
(101) GCAATAATTA TCTGAATTGG TACCTTCAAA AACCAGGTCA AAGCCCGCAG
(151) CTATTAATTT ATCTTGGTTC TAATCGTGCC AGTGGGGTCC CGGATCGTTT
(201) TAGCGGCTCT GGATCCGGCA CCGATTTTAC CCTGAAAATT AGCCGTGTGG
(251) AAGCTGAAGA CGTGGGCGTG TATTATTGCC AGCAGTATTC TTCTAAGTCT
(301) GCTACCTTTG GCCAGGGTAC GAAAGTTGAA ATTAAACGTA CG
```

3079_Vk kappa 1 (SEQ ID NO: 10):

```
(1)  GATATCCAGA TGACCCAGAG CCCGTCTAGC CTGAGCGCGA GCGTGGGTGA
(51) TCGTGTGACC ATTACCTGCA GAGCGAGCCA GGATATTTCT GCTTTTCTGA
(101) ATTGGTACCA GCAGAAACCA GGTAAAGCAC CGAAACTATT AATTTATAAG
(151) GTTCTAATT TGCAAAGCGG GGTCCCGTCC CGTTTTAGCG GCTCTGGATC
(201) CGGCACTGAT TTTACCCTGA CCATTAGCAG CCTGCAACCT GAAGACTTTG
(251) CGACTTATTA TTGCCAGCAG GCTTATTCTG GTTCTATTAC CTTTGGCCAG
(301) GGTACGAAAG TTGAAATTAA ACGTACG
```

3080_VI lambda 3 (SEQ ID NO: 11):

```
(1)  GATATCGAAC TGACCCAGCC GCCTTCAGTG AGCGTTGCAC CAGGTCAGAC
(51) CGCGCGTATC TCGTGTAGCG GCGATAATAT TGGTAATAAG TATGTTTCTT
(101) GGTACCAGCA GAAACCCGGG CAGGCGCCAG TTGTTGTGAT TTATGGTGAT
(151) AATAATCGTC CCTCAGGCAT CCCGGAACGC TTTAGCGGAT CCAACAGCGG
(201) CAACACCGCG ACCCTGACCA TTAGCGGCAC TCAGGCGGAA GACGAAGCGG
(251) ATTATTATTG CTCTTCTTAT GATTCTTCTT ATTTTGTGTT TGGCGGCGGC
(301) ACGAAGTTAA CCGTTCTTGG CCAG
```

3100_VI lambda 3 (SEQ ID NO: 12):

```
(1)  GATATCGAAC TGACCCAGCC GCCTTCAGTG AGCGTTGCAC CAGGTCAGAC
(51) CGCGCGTATC TCGTGTAGCG GCGATAATAT TGGTCATTAT TATGCTTCTT
(101) GGTACCAGCA GAAACCCGGG CAGGCGCCAG TTCTTGTGAT TTATCGTGAT
(151) AATGATCGTC CCTCAGGCAT CCCGGAACGC TTTAGCGGAT CCAACAGCGG
(201) CAACACCGCG ACCCTGACCA TTAGCGGCAC TCAGGCGGAA GACGAAGCGG
(251) ATTATTATTG CCAGTCTTAT GATTATCTTC ATGATTTTGT GTTTGGCGGC
(301) GGCACGAAGT TAACCGTTCT TGGCCAG
```

Figure 2b**Variable Light Chain Peptide****(CDR Regions in Bold)****3077_Vk kappa 2 (SEQ ID NO: 13):**

(1) DIVMTQSPLS LPVTPGEPAS ISCRSSQSLL **FIDGNNYLNW** YLQKPGQSPQ
(51) **LLIYLG**SNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV **YYCQQYSSKS**
(101) ATFGQGTKVE IKRT

3079_Vk kappa 1 (SEQ ID NO: 14):

(1) DIQMTQSPSS LSASVGDRVIT ITCRASQDIS **AFLN**WYQQKP GKAPKLLIYK
(51) **VSNLQSG**VPS RFSGSGSGTD FTLTISSLPQ EDFATYYCQQ **AYSGSIT**FGQ
(101) GTKVEIKRT

3080_Vl lambda 3 (SEQ ID NO: 15):

(1) DIELTQPPSV SVAPGQTARI SCSGDNIGNK **YVSWYQQKPG** QAPVVVIYGD
(51) **NNRPSG**IPER FSGSNSGNTA TLTISGTQAE DEADYYCSSY **DSSYFV**FGGG
(101) TKLTVLGQ

3100_Vl lambda 3 (SEQ ID NO: 16):

(1) DIELTQPPSV SVAPGQTARI SCSGDNIGHY **YASWYQQKPG** QAPVLVIYRD
(51) **NDRPSG**IPER FSGSNSGNTA TLTISGTQAE DEADYYCQSY **DYLHDFV**FGG
(101) GTKLTVLGQ

Figure 3**Variable Heavy Chain Consensus Sequences**(CDR Regions in **Bold**)**VH1B Consensus (SEQ ID NO: 17):**

(1) QVQLVQSGAE VKKPGASVKV SCKAS**GYTFT** **SYMHWVRQA** PGQGLEWMGW
(51) **INPNSGGTNY** **AQKFQGRVTM** TRDTSISTAY MELSSLRSED TAVYYCAR**WG**
(101) **GDGFYAMDYW** GQGTILVTVSS

VH3 Consensus (SEQ ID NO: 18):

(1) QVQLVESGGG LVQPGGSLRL SCAAS**GFTFS** **SYAMSWVRQA** PGKGLEWVSA
(51) **ISGSGGSTYY** **ADSVKGRFTI** SRDNSKNTLY LQMNSLRAED TAVYYCAR**WG**
(101) **GDGFYAMDYW** GQGTILVTVS S

Figure 4**Variable Light Chain Consensus Sequences**(CDR Regions in **Bold**)**VL_λ3 Consensus (SEQ ID NO: 19):**

(1) SYELTQPPSV SVAPGQTARI **SCSGDALGDK YASWYQQKPG** QAPVLVIYDD
(51) **SDRPSGIPER** FSGSNSGNTA TLTISGTQAE DEADYYC**QQH YTT**PPVFGGG
(101) TKLTVLG

VL_k1 Consensus (SEQ ID NO: 20):

(1) DIQMTQSPSS LSASVGDRVIT ITCRAS**QGIS SYLAWYQQKPG** GKAPKLLIYA
(51) **ASSLQSGVPS** RFGSGSGTD FTLTISSLQP EDFATYYC**QQ HY**TTTPPTFGQ
(101) GTKVEIKR

VL_k2 Consensus (SEQ ID NO: 21):

(1) DIVMTQSPLS LPVTPGEPAS ISCRSS**QSL**L **HSNGYNYLDW** YLQKPGQSPQ
(51) **LLIYLGSNRA** SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYC**QQHY**TTTP
(101) PTFGQGTKVE IKR

Figure 5**Peptide Sequence of CD38**

(SEQ ID NO: 22):

```
1      mancefspvs gdkpccrlsr raqlclgvs l vlilvvla vvvprwrqqw sgpgttkrfp
61     etvlarcvky teihpemrhv dcqsvdafk gafiskhpcn iteedyqplm klgtqtvpcn
121    killwsrikd lahqftqvqr dmftledtll gyladdltwc gefntskiny qscpdwrkdc
181    snnpvsvfwk tvsrrfaaaa cdvvhvmlng srskifdkns tfgsvevhn1 qpekvtlea
241    wvihggregs rdlcqdptik elesiiskrn iqfsckniyr pdkflqcvkn pedssctsei
```


Figure 6**Nucleotide Sequence of Chimeric OKT10**

Heavy Chain (SEQ ID NO: 23):

cagggtggaat tgggtggaatc tggaggatcc ctgaaactct cctgtgcagc ctcaggattc
gatttttagta gatcctggat gaattgggtc cggcaggctc caggaaaagg gctagaatgg
attggagaaa ttaatccaga tagcagtacg ataaactata cgacatctct aaaggataaa
ttcatcatct ccagagacaa cgccaaaaat acgctgtacc tgcaaatgac caaagtgaga
tctgaggaca cagcccttta ttactgtgca agatatggta actggtttcc ttattggggc
caagggactc tggtcactgt cagctcagcc tccaccaagg gtccatcggc cttccccctg
gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac
tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac
accttccccg ctgtcctaca gtctcagga ctctactccc tcagcagcgt ggtgaccgtg
ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcacia gccagcaac
accaaggtgg acaagaaagt tgagcccaaa tcttgtgaca aaactcacac atgccaccg
tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc aaaaccaag
gacaccctca tgatctcccg gaccctgag gtcacatgcg tggtggtgga cgtgagccac
gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaa
acaaagccgc gggaggagca gtacaacagc acgtaccggg tggtcagcgt cctcacctc
ctgcaccagg actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc
ccagccccc tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg
tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgctg
gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag
aacaactaca agaccacgcc tcccgtgctg gactccgacg gtccttctt cctctacagc
aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg
catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaa

Light Chain (SEQ ID NO: 24):

gatatcctga tgaccagtc tcaaaaaatc atgccacat cagtgggaga cagggtcagc
gtcacctgca aggcagtc aaatgtggat actaatgtag cctggatatca acagaaacca

ggacagtctc ctaaagcact gatttactcg gcacccctacc gatacagtgg agtccctgat
cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcaccaa tgtgcagtct
gaggacttgg cagagtatct ctgtcagcaa tatgacagct atcctctcac gttcgggtgct
gggaccaagc tggacctgaa acgtacggtg gctgcacat ctgtcttcat cttcccgcca
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt

Fig.7: Schematic Overview of Epitopes

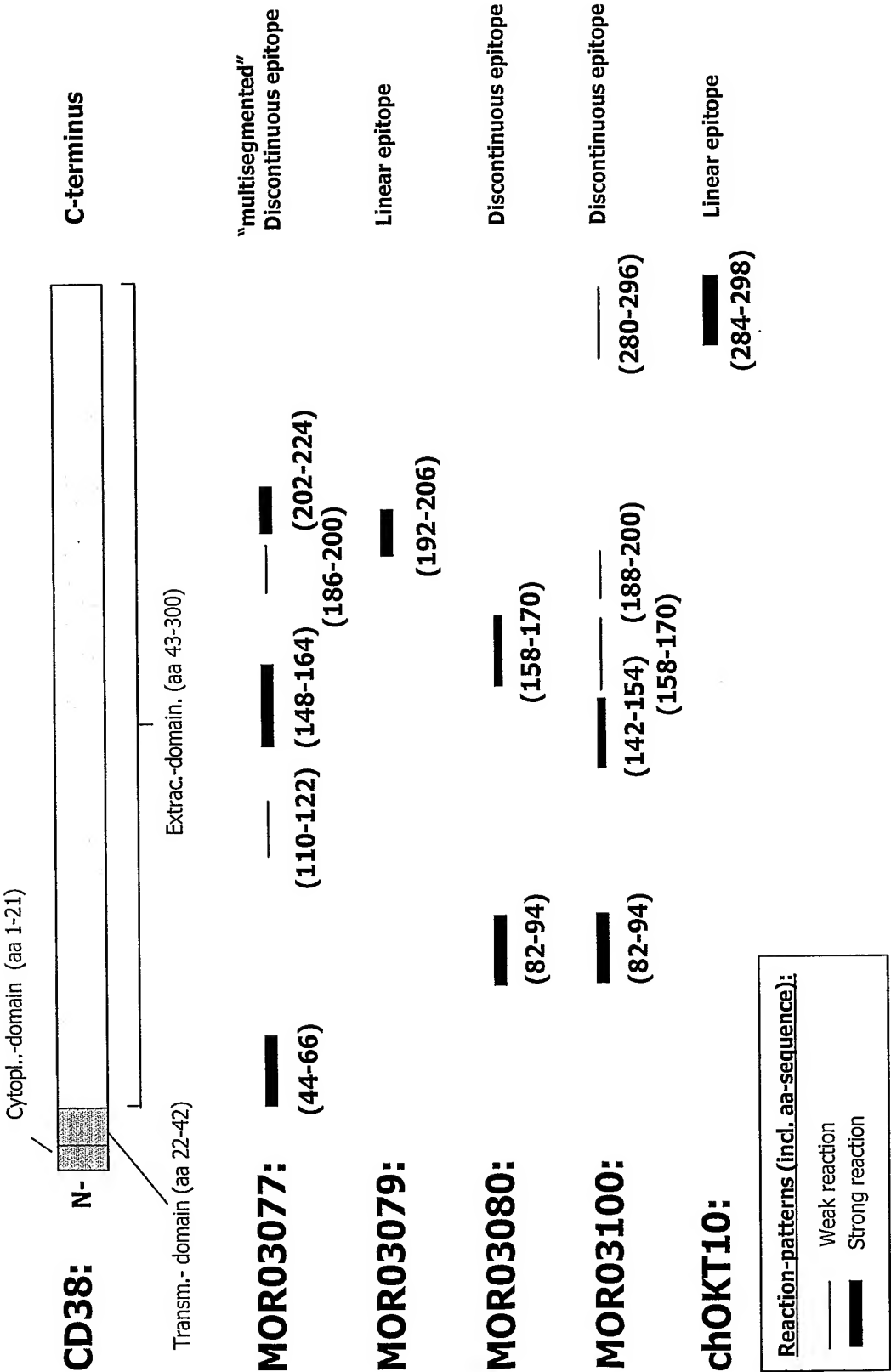


Figure 8: DNA sequence of pMOPRH[®]_h_IgG1_1

```

                StyI
                ~~~~~
601   TCGCTATTAC CATGGTGATG CGGTTTTTGGC AGTACATCAA TGGGCGTGGA
      AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT

                                           AatII
                                           ~~~~~
651   TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
      ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

701   TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA
      ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT

751   ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG
      TGTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC

801   GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
      CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTTGGGT GACGAATGAC

                pMORPH®_Ig_FOR 100.0%
                ~~~~~
851   GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
      CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGTT CGACCGATCG

                M K H L W F F L L L V A A P R

901   GCCACCATGA AACACCTGTG GTTCTTCCTC CTGCTGGTGG CAGCTCCAG
      CGGTGGTACT TTGTGGACAC CAAGAAGGAG GACGACCACC GTCGAGGGTC

                EcoRI
                ~~~~~
                StyI
                ~~~~~
                BspI
                ~~~~~
                BlpI
                ~~~~~
                A S T

      · W V L S Q V E F C R R L A Q
951   ATGGGTCCTG TCCCAGGTGG AATTCTGCAG GCGGTTAGCT CAGCCTCCAC
      TACCCAGGAC AGGGTCCACC TTAAGACGTC CGCCAATCGA GTCGAGGGTG

      StyI
      ~~~~~
      · K G P S V F P L A P S S K S T S G

1001  CAAGGGTCCA TCGGTCTTCC CCCTGGCACC CTCCTCCAAG AGCACCTCTG
      GTTCCCAGGT AGCCAGAAGG GGGACCGTGG GAGGAGGTTT TCGTGGAGAC

      · G T A A L G C L V K D Y F P E P
1051  GGGGCACAGC GGCCCTGGGC TGCCTGGTCA AGGACTACTT CCCCGAACCG
      CCCCCTGTCG CCGGGACCCG ACGGACCAGT TCCTGATGAA GGGGCTTGGC

```

V T V S W N S G A L T S G V H T F
 1101 GTGACGGTGT CGTGGAAGTC AGGCGCCCTG ACCAGCGGCG TGCACACCTT
 CACTGCCACA GCACCTTGAG TCCGCGGGAC TGGTCGCCGC ACGTGTGGAA
 . P A V L Q S S G L Y S L S S V V T
 1151 CCCGGCTGTC CTACAGTCCT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA
 GGGCCGACAG GATGTCAGGA GTCCTGAGAT GAGGGAGTCG TCGCACCCT
 . V P S S S L G T Q T Y I C N V N
 1201 CCGTGCCCTC CAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT
 GGCACGGGAG GTCGTCGAAC CCGTGGGTCT GGATGTAGAC GTTGCACCTTA
 StyI
 ~~~~~  
 H K P S N T K V D K K V E P K S C  
 1251 CACAAGCCCA GCAACACCAA GGTGGACAAG AAAGTTGAGC CCAAATCTTG  
 GTGTTCCGGT CGTTGTGGTT CCACCTGTTC TTTCAACTCG GGTTTAGAAC  
 . D K T H T C P P C P A P E L L G G  
 1301 TGACAAAACCT CACACATGCC CACCGTGCCC AGCACCTGAA CTCCTGGGGG  
 ACTGTTTTGA GTGTGTACGG GTGGCACGGG TCGTGGACTT GAGGACCCCC  
 BbsI StyI  
 ~~~~~  
 . P S V F L F P P K P K D T L M I
 1351 GACCGTCAGT CTTCTCTTTC CCCCCAAAAC CCAAGGACAC CCTCATGATC
 CTGGCAGTCA GAAGGAGAAG GGGGGTTTTG GGTTCCTGTG GGAGTACTAG
 BbsI
 ~~~~~  
 S R T P E V T C V V V D V S H E D  
 1401 TCCCGGACCC CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA  
 AGGGCCTGGG GACTCCAGTG TACGCACCAC CACCTGCACT CGGTGCTTCT  
 BbsI  
 ~~~~~  
 . P E V K F N W Y V D G V E V H N A
 1451 CCCTGAGGTC AAGTTCAACT GGTACGTGGA CGGCGTGGAG GTGCATAATG
 GGGACTCCAG TTCAAGTTGA CCATGCACCT GCCGCACCTC CACGTATTAC
 . K T K P R E E Q Y N S T Y R V V
 1501 CCAAGACAAA GCCGCGGGAG GAGCAGTACA ACAGCACGTA CCGGGTGGTC
 GTTCTGTTT CGGCGCCCTC CTCGTCATGT TGTCTGTCAT GGCCACCAG
 S V L T V L H Q D W L N G K E Y K
 1551 AGCGTCCTCA CCGTCCTGCA CCAGGACTGG CTGAATGGCA AGGAGTACAA
 TCGCAGGAGT GGCAGGACGT GGTCTGACC GACTTACCGT TCCTCATGTT
 . C K V S N K A L P A P I E K T I S
 1601 GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG AAAACCATCT
 CACGTTCCAG AGGTTGTTTC GGGAGGGTCG GGGGTAGCTC TTTTGGTAGA

```

                                BsrGI
                                ~~~~~
      . K A K   G Q P   R E P Q   V Y T   L P P
1651 CCAAAGCCAA AGGGCAGCCC CGAGAACCAC AGGTGTACAC CCTGCCCCCA
      GGTTCGGTT TCCCGTCGGG GCTCTTGGTG TCCACATGTG GGACGGGGGT

      S R D E   L T K   N Q V   S L T C   L V K

      .
1701 TCCCGGGATG AGCTGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA
      AGGGCCCTAC TCGACTGGTT CTTGGTCCAG TCGGACTGGA CGGACCAGTT

      . G F Y   P S D I   A V E   W E S   N G Q P

      .
1751 AGGCTTCTAT CCCAGCGACA TCGCCGTGGA GTGGGAGAGC AATGGGCAGC
      TCCGAAGATA GGGTCGCTGT AGCGGCACCT CACCCTCTCG TTACCCGTCG

      . E N N   Y K T   T P P V   L D S   D G S
1801 CGGAGAACAA CTACAAGACC ACGCCTCCCG TGCTGGACTC CGACGGCTCC
      GCCTCTTGTT GATGTTCTGG TCGGGAGGGC ACGACCTGAG GCTGCCGAGG

      F F L Y   S K L   T V D   K S R W   Q Q G

      .
1851 TTCTTCCTCT ACAGCAAGCT CACCGTGGAC AAGAGCAGGT GGCAGCAGGG
      AAGAAGGAGA TGTCGTTCTGA GTGGCACCTG TTCTCGTCCA CCGTCGTCCC

      BbsI                      NsiI
      ~~~~~                      ~~~~~
      . N V F   S C S V   M H E   A L H   N H Y T

      .
1901 GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC AACCACTACA
      CTTGCAGAAG AGTACGAGGC ACTACGTACT CCGAGACGTG TTGGTGATGT

      SapI                      PmeI
      ~~~~~                      ~~~~~
      . Q K S   L S L   S P G K   *
1951 CGCAGAAGAG CCTCTCCCTG TCTCCGGGTA AATGAGGGCC CGTTTAAACC
      GCGTCTTCTC GGAGAGGGAC AGAGGCCCAT TTACTCCCGG GCAAATTTGG

      2001 CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG
      GCGACTAGTC GGAGCTGACA CGGAAGATCA ACGGTCGGTA GACAACAAAC

      ~~~~~
      pMORPH®_Ig_REV 100.0%
2051 CCCCTCCCCC GTGCCTTCCT TGACCCTGGA AGGTGCCACT CCCACTGTCC
      GGGGAGGGGG CACGGAAGGA ACTGGGACCT TCCACGGTGA GGGTGACAGG

```



```
+1  A S V V C L L N N F Y P R E A K V
1051 GCCTCTGTTG TGTGCCCTGCT GAATAACTTC TATCCCAGAG AGGCCAAAGT
    CCGAGACAAC ACACGGACGA CTTATTGAAG ATAGGGTCTC TCCGGTTTCA

+1  Q W K V D N A L Q S G N S Q E S
1101 ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC CAGGAGAGTG
    TGTACCTTC CACCTATTGC GGGAGGTTAG CCCATTGAGG GTCCTCTCAC

+1  V T E Q D S K D S T Y S L S S T L
1151 TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCTTG
    AGTGTCCTCGT CCTGTCGTTC CTGTCGTGGA TGTGCGAGTC GTCGTGGGAC

+1  T L S K A D Y E K H K V Y A C E V
    BlpI
    ~~~~~
1201 ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT
    TCGACTCGT TTCGTCTGAT GCTCTTTGTG TTTCAGATGC GGACGCTTCA

+1  T H Q G L S S P V T K S F N R G
1251 CACCCATCAG GGCCTGAGCT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG
    GTGGGTAGTC CCGGACTCGA GCGGGCAGTG TTTCTCGAAG TTGTCCCCTC

+1  E C *
                                PmeI
                                ~~~~~
                                pMORPH®_Ig_REV 100%
                                =====
1301 AGTGTTAGGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT
    TCACAATCCC CGGGCAAATT TGGGCGACTA GTCGGAGCTG ACACGGAAGA

=
1351 AGTTGCCAGC CATCTGTTGT TTGCCCCTCC CCCGTGCCTT CCTTGACCCT
    TCAACGGTCG GTAGACAACA AACGGGGAGG GGGCACGGAA GGAAGTGGGA
```


Figure 10: DNA Sequence of HuCAL[®] Ig lambda light chain vector
pMORPH[®]_h_Igλ_1

```

                StyI
                ~~~~~~
601  TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA
    AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT ACCCGCACCT

651  TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
    ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

701  TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA
    ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT

751  ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG
    TGTTGAGGCG GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC

801  GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG
    CAGATATATT CGTCTCGAGA GACCGATTGA TCTCTTGGGT GACGAATGAC

                pM_Ig_FOR 100.0%
                =====
                ~~~~~~
851  GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
    CGAATAGCTT TAATTATGCT GAGTGATATC CCTCTGGGTT CGACCGATCG

+1      M A W A L L L L T L L T Q G T
        StyI
        ~~~~~~
901  GCCACCATGG CCTGGGCTCT GCTGCTCCTC ACCCTCCTCA CTCAGGGCAC
    CCGTGGTACC GGACCCGAGA CGACGAGGAG TGGGAGGAGT GAGTCCCGTG

+2      T V L G Q
+1      G S W A D I V M H E V
        BamHI      EcoRV      HpaI      StyI
        ~~~~~~
951  AGGATCCTGG GCTGATATCG TGATGCACGA AGTTAACCGT CCTAGGTCAG
    TCCTAGGACC CGACTATAGC ACTACGTGCT TCAATTGGCA GGATCCAGTC

+2      P K A A P S V T L F P P S S E E L
        StyI
        ~~~~~~
1001 CCCAAGGCTG CCCCTCGGT CACTCTGTTC CCGCCCTCCT CTGAGGAGCT
    GGGTTCCGAC GGGGGAGCCA GTGAGACAAG GCGGGGAGGA GACTCCTCGA

+2      Q A N K A T L V C L I S D F Y P
1051 TCAAGCCAAC AAGGCCACAC TGGTGTGTCT CATAAGTGAC TTCTACCCGG
    AGTTCGGTTG TTCCGGTGTG ACCACACAGA GTATTCAGTG AAGATGGGCC

```

```
+2 G A V T V A W K G D S S P V K A G
1101 GAGCCGTGAC AGTGGCCTGG AAGGGAGATA GCAGCCCCGT CAAGGCGGGA
      CTCGGCACTG TCACCGGACC TTCCCTCTAT CGTCGGGGCA GTTCCGCCCT

+2 V E T T T P S K Q S N N K Y A A S
1151 GTGGAGACCA CCACACCCCTC CAAACAAAGC AACAAACAAGT ACGCGGCCAG
      CACCTCTGGT GGTGTGGGAG GTTTGTTTCG TTGTTGTTCA TGCGCCGGTC

+2 S Y L S L T P E Q W K S H R S Y
1201 CAGCTATCTG AGCCTGACGC CTGAGCAGTG GAAGTCCCAC AGAAGCTACA
      GTCGATAGAC TCGGACTGCG GACTCGTCAC CTTCAGGGTG TCTTCGATGT

+2 S C Q V T H E G S T V E K T V A P
      BbsI
      ~~~~~
1251 GCTGCCAGGT CACGCATGAA GGGAGCACCG TGGAGAAGAC AGTGGCCCCCT
      CGACGGTCCA GTGCGTACTT CCCTCGTGGC ACCTCTTCTG TCACCGGGGA

+2 T E C S *
      PmeI
      ~~~~~
1301 ACAGAATGTT CATAGGGGCC CGTTTAAACC CGCTGATCAG CCTCGACTGT
      TGTCTTACAA GTATCCCCGG GCAAATTTGG GCGACTAGTC GGAGCTGACA
      pM_Ig_REV 100%
      =====

1351 GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCTCCCCC GTGCCTTCCT
      CGGAAGATCA ACGGTCGGTA GACAACAAAC GGGGAGGGGG CACGGAAGGA
      pM_Ig_REV 100.0%
      =====
```


Fig. 12: IL-6 Release Assay

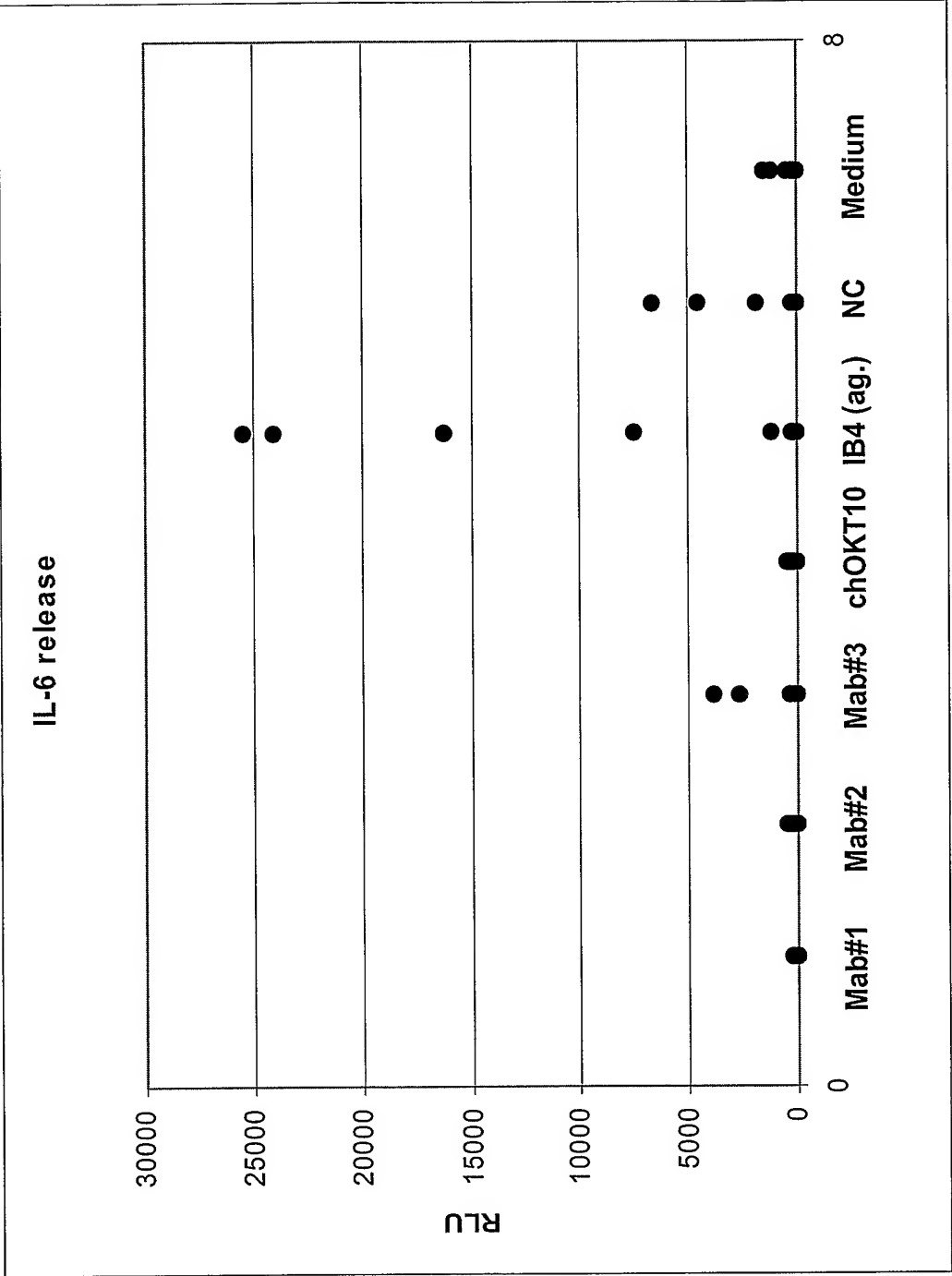


Fig. 13: Cytotoxicity towards CD34+/CD38+ progenitor cells

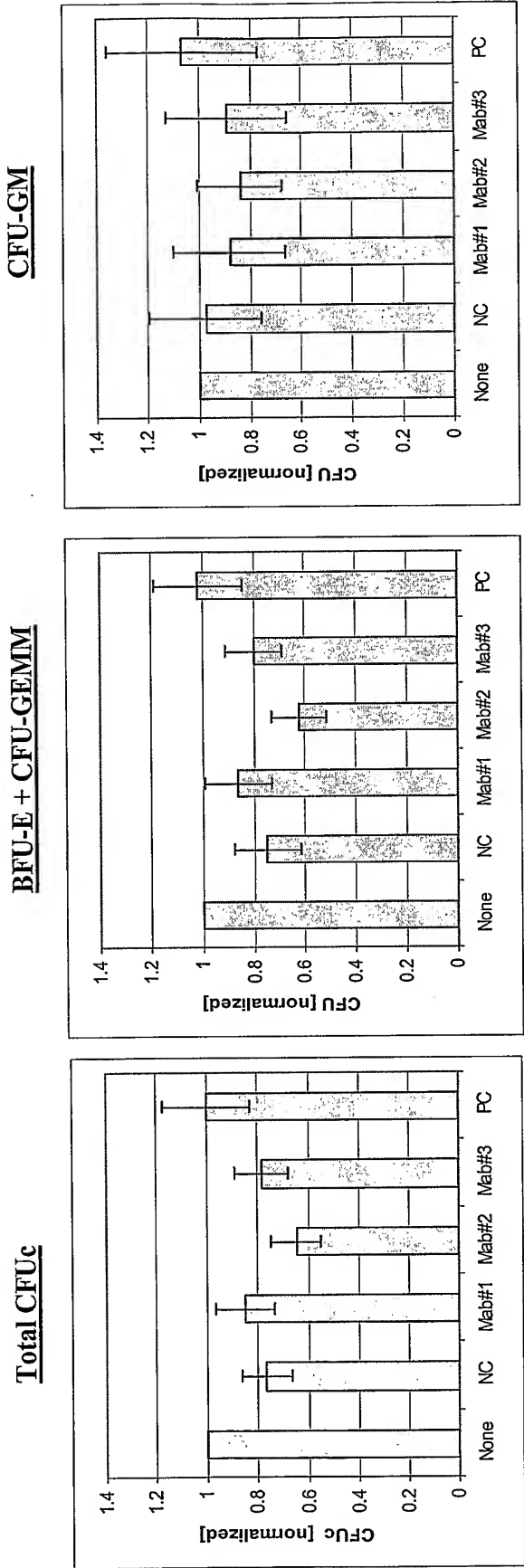


Fig. 14: ADCC with different cell-lines

Cell line	Culture Collection	Origin	Expression [MFI]	Max. specific killing [%] in ADCC ^{a,c}			
				Mab#1	Mab#2	Mab#3	PC
RPMI 8226	ATCC CCL-155	MM	405.71	56	58	54	46
KMS-12-BM	DSMZ ACC551	MM	142.29	26	32	30	34
NCI-H929	ECACC95050415	MM	45.01	68	73	38	54
OPM-2	DSMZ ACC50	MM	37.99	6	13	3	7
U-266	ECACC85051003	MM	26.14	17	14	12	16
KMS-11	Namba <i>et al.</i> , 1989 ^b	MM	26.81 ^d	22	30	26	28
JVM-13	DSMZACC19	CLL	463.93	11	20	12	15
JVM-2	DSMZACC12	CLL	140.84	22	28	10	24
CCRF-CEM	ECACC85112105	ALL	301.46	24	29	20	22
Jurkat	DSMZ ACC282	ALL	202.99	7	8	13	12
AML-193	DSMZ ACC549	AML	62.69 ^d	33	26	39	33
OCI-AML5	DSMZ ACC247	AML	207.55 ^d	20	21	16	26
NB-4	DSMZ ACC207	AML	164.7 ^d	36	38	32	37
THP-1	DSMZ ACC16	AML	34.41	64	59	38	43
HL-60 ^d	DSMZ ACC3	AML	18.43 ^d	29	35	29	29
Raji	Burkitt's Lymph.	Burkitt's lymph.	n.d.	53	62	48	n.d.

Fig. 15: ADCC with MM-samples

Antibodies		Mab#1	Mab#2	Mab#3	PC
Parameters:					
MM samples: EC50 [nM] ^a :		0.116-0.202	0.006-0.185	0.027-0.249	0.282-0.356
MM samples: Max spec. killing [%]		13.1 - 61.6	16.2 - 57.9	13.6 - 36.0	15.5 - 49.5

Fig. 16: Treatment of human myeloma xenograft with MOR03080

